

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 18:56:08 ; Search time 893 Seconds  
(without alignments)  
10481.989 Million cell updates/sec

Title: US-09-727-628-3

Perfect score: 2069  
Sequence: 1 ttatagattttttcaattc.....gggaattaaggaaccattgg 2069

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2937390 seqs, 2262062796 residues

Total number of hits satisfying chosen parameters: 5874780

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database : Published Applications NA:

- 1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:
- 2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:
- 3: /cgn2\_6/prodata/1/pubpna/US05\_NEW\_PUB.seq:
- 4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:
- 5: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:
- 6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq:
- 7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:
- 8: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:
- 9: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq:
- 10: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:
- 14: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:
- 15: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:
- 16: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:
- 17: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:
- 18: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:
- 19: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2069	100.0	2069	9	US-09-727-628-3
2	187.8	9.1	1971	13	Sequence 3, Appl1
3	123	5.9	1912	13	Sequence 26983, A
4	120	5.8	1914	13	Sequence 8483, Ap
5	119	5.8	1879	13	Sequence 5612, Ap
6	118.8	5.7	2156	13	Sequence 5704, Ap
7	118.8	5.7	2156	13	Sequence 1, Appl1
8	105.2	5.1	753	15	Sequence 25858, A
9	82.6	4.0	280	9	Sequence 43, Appl1
10	82.6	3.0	6881	15	Sequence 601, App
11	62.8	3.0	6881	15	Sequence 1354, Ap
12	58.8	2.8	3673778	15	Sequence 124, App
13	53	2.6	5362	15	Sequence 1, Appl1
14	52.2	2.5	19380	13	Sequence 287, App
					Sequence 390, App

#### ALIGNMENTS

##### RESULT 1

US-09-727-628-3  
; Sequence 3, Application US/09727628  
; Patent No. US20020068359A1  
; GENERAL INFORMATION:  
; APPLICANT: Armstrong, Katherine  
; APPLICANT: Hey, Timothy D  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Smith, Kelley A  
; APPLICANT: Hopkins, Nicole L  
; TITLE OF INVENTION: MAIZE MIP SYNTHASE PROMOTER  
; FILE REFERENCE: 50597  
; CURRENT APPLICATION NUMBER: US/09/727,628  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/168,612  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-727-628-3

Query Match	100.0%	Score 2069;	DB 9;	Length 2069;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2069;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

QY	1	TCTAGATTTTTTTCATTCACCCGAGTAATTCGAATCCAAATCACAATCTTAAAAATCAGGAG	60
Db	1	TCTAGATTTTTTTCATTCACCCGAGTAATTCGAATCCAAATCACAATCTTAAAAATCAGGAG	60
QY	61	AAATTTATATGCGCATTTATATAGAACCAACTAAATAAATGTCGGTTGTTATTGAAAAAAA	120
Db	61	AAATTTATATGCGCATTTATATAGAACCAACTAAATAAATGTCGGTTGTTATTGAAAAAAA	120
QY	121	ACCTATTATACAAAAACATCTGCCAAGAATACAAATCTTTTATATACACAACTTATATGTGA	180

Db 121 ACCTATTTTAAACAAACATCTGCCAAGAATACAAATCTTTTATACAAACTTATATGTA 180  
QY 181 GTTCTTTTCTCTGTAACTCTTATTAATAAACAATTTTGGCTATTAATAATGCGAAC 240  
Db 181 GTTCTTTTCTCTGTAACTCTTATTAATAAACAATTTTGGCTATTAATAATGCGAAC 240  
QY 241 TAGTTAGACCACTGTAATAGATTTTGTCTGGAACAATTTCTCTGACTAGAGACTAT 300  
Db 241 TAGTTAGACCACTGTAATAGATTTTGTCTGGAACAATTTCTCTGACTAGAGACTAT 300  
QY 301 TTGGACTGTCTTTTGGCAACCAAGTAGAAATGGAACCGCTCTTTTAAACCACTTCTC 360  
Db 301 TTGGACTGTCTTTTGGCAACCAAGTAGAAATGGAACCGCTCTTTTAAACCACTTCTC 360  
QY 361 ACATCGTGGTCTGTAATAGATTTTGTCTGGAACAATTTCTCTGACTAGAGACTAT 420  
Db 361 ACATCGTGGTCTGTAATAGATTTTGTCTGGAACAATTTCTCTGACTAGAGACTAT 420  
QY 421 TAGTATGTGTTTATAAATCAATTTTACCAATTTTAAATAAATGTAAGTATTTTCA 480  
Db 421 TAGTATGTGTTTATAAATCAATTTTACCAATTTTAAATAAATGTAAGTATTTTCA 480  
QY 481 TCAGTAGAACTACTACGAGAGCTTAAACAAACAAAGTGTCTTACTGATAAAGCAGAGA 540  
Db 481 TCAGTAGAACTACTACGAGAGCTTAAACAAACAAAGTGTCTTACTGATAAAGCAGAGA 540  
QY 541 TGATGTATGACCGTGACCGTGAGCTTAAAGTCCAAACAAACAAACAAACAAACAAAC 600  
Db 541 TGATGTATGACCGTGAGCGTGAGCTTAAAGTCCAAACAAACAAACAAACAAACAAAC 600  
QY 601 CAAACAAAGTGTATGTATGATGCTTAAATTAAGCAGACAGTACACACAGTATATTAT 660  
Db 601 CAAACAAAGTGTATGTATGATGCTTAAATTAAGCAGACAGTACACACAGTATATTAT 660  
QY 661 TCTCTCTCCATATACAGAGTATGCTGTAAGTAAATTTTGTATGTAAGTAAATTTAGTA 720  
Db 661 TCTCTCTCCATATACAGAGTATGCTGTAAGTAAATTTTGTATGTAAGTAAATTTAGTA 720  
QY 721 AATAATGCTAGCTTACGTTACGGAATTTATGGAATAATGTAATTTGTTTATATA 780  
Db 721 AATAATGCTAGCTTACGTTACGGAATTTATGGAATAATGTAATTTGTTTATATA 780  
QY 781 ATTTTATATAAATGTAATGCTGTTCTGTTCTGATGAGGATTAATAGTCAATA 840  
Db 781 ATTTTATATAAATGTAATGCTGTTCTGTTCTGATGAGGATTAATAGTCAATA 840  
QY 841 CGAATGGGAACACCAACCAACCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 CGAATGGGAACACCAACCAACCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
QY 901 TGCCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Db 901 TGCCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
QY 961 GGACAAGAGTCTTTTACATGCAAGGACAAATAAATCTCCACGCGGCCCAACCGTCTTGGCA 1020  
Db 961 GGACAAGAGTCTTTTACATGCAAGGACAAATAAATCTCCACGCGGCCCAACCGTCTTGGCA 1020  
QY 1021 AGCCACATGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
Db 1021 AGCCACATGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
QY 1081 GTGAGTCTGACACCGCACCAATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
Db 1081 GTGAGTCTGACACCGCACCAATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
QY 1141 GTGTTGCGAGGCTCTGCGCGCTTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
Db 1141 GTGTTGCGAGGCTCTGCGCGCTTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
QY 1201 TCCTTAGGGGCGAGGAGTGTGACCGCACCAAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1260

Db 1201 TCCTTAGGGGCGAGGAGTGTGACCGCACCAAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
QY 1261 GAGCGGGGCTAACCCAGGAGCTTCCGCCAGCTTGGAGACCAAGTACGCGGCGAGAGGAGC 1320  
Db 1261 GAGCGGGGCTAACCCAGGAGCTTCCGCCAGCTTGGAGACCAAGTACGCGGCGAGAGGAGC 1320  
QY 1321 TCCACGGGATCAAAAAGCGCGCCACTTCTTAAAGGTCAAGGGTCTTGGCTTCTGCGCTTCTG 1380  
Db 1321 TCCACGGGATCAAAAAGCGCGCCACTTCTTAAAGGTCAAGGGTCTTGGCTTCTGCGCTTCTG 1380  
QY 1381 GTGCTTCTTCAAAATCTGGAACCTAGTGGATCAATTTAGTACACCTCAGCAACCGATGC 1440  
Db 1381 GTGCTTCTTCAAAATCTGGAACCTAGTGGATCAATTTAGTACACCTCAGCAACCGATGC 1440  
QY 1441 AGCCAGATGATGACGACGATTTGTGACGCTGTGGGGTCAATGCTCAATGCAACCGAGCA 1500  
Db 1441 AGCCAGATGATGACGACGATTTGTGACGCTGTGGGGTCAATGCTCAATGCAACCGAGCA 1500  
QY 1501 CGAATTTGGTGTCTGCTTCTTGTACACGCTAGTACGATTTGATTTGATTTCAATTTG 1560  
Db 1501 CGAATTTGGTGTCTGCTTCTTGTACACGCTAGTACGATTTGATTTGATTTCAATTTG 1560  
QY 1561 AACTGTTTAAACTTATATATGAGAAATTAGTCAAACTCATGCTTAAATAAAAGTATA 1620  
Db 1561 AACTGTTTAAACTTATATATGAGAAATTAGTCAAACTCATGCTTAAATAAAAGTATA 1620  
QY 1621 AAACCCATCGAATTTATGATGATGAGAGATTTAGTCAAACTCATGCTTAAATAAAAGTATA 1680  
Db 1621 AAACCCATCGAATTTATGATGATGAGAGATTTAGTCAAACTCATGCTTAAATAAAAGTATA 1680  
QY 1681 TCACAGAGTACGACCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
Db 1681 TCACAGAGTACGACCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
QY 1741 ATGCTGGGCTCAGCAAAAGTTCCGGGCTTCCGGCAATTCGGCGGCGCGGCTGCGGCTCAA 1800  
Db 1741 ATGCTGGGCTCAGCAAAAGTTCCGGGCTTCCGGCAATTCGGCGGCGCGGCTGCGGCTCAA 1800  
QY 1801 ATCCGATCTACCGCGGCTAGAGCT 1860  
Db 1801 ATCCGATCTACCGCGGCTAGAGCT 1860  
QY 1861 CTTTCAATTTGGGAGTGGCGCTCTCGAACCCTCTATAAATCCCGGCGCGGCGGCGGCGGCGG 1920  
Db 1861 CTTTCAATTTGGGAGTGGCGCTCTCGAACCCTCTATAAATCCCGGCGCGGCGGCGGCGGCGG 1920  
QY 1921 TCCCGGACCAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1980  
Db 1921 TCCCGGACCAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1980  
QY 1981 TCTCTCGGCGGCGGCTCGCTTACCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 2040  
Db 1981 TCTCTCGGCGGCGGCTCGCTTACCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 2040  
QY 2041 GAGAGGAGGAGGAGTAAAGGCAACCATGG 2069  
Db 2041 GAGAGGAGGAGGAGTAAAGGCAACCATGG 2069

## RESULT 2

US-10-425-114-26983  
; Sequence 26983, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B

```

RESULT 4
US-10-425-114-5612
; Sequence 5612, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5612
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700466493_FLI
US-10-425-114-5612

Query Match          5.8%; Score 120; DB 13; Length 1914;
Best Local Similarity 98.5%; Pred. No. 3.le-19; Indels 2; Gaps 1;
Matches 132; Conservative 0; Mismatches 0;

QY      1930 ACACAGCCCAACAACAGGAGCGCGGGGCCCTCCTTCCTTCCCTCCCACATTCTCTGC 1989
DB      1   ACACAGCCCAACA--AAGGAGCGCGGGGCCCTCCTTCCTTCCCTCCCACATTCTCTGC 58

QY      1990 CGGCGCTCGCTTACTTCGTCCATCCGTTCCGAGCAGGAGCGGAGTGAGAAGGGA 2049
DB      59  CGGCGCTCGCTTACTTCGTCCATTCGATTCGATTCGAGGAGGCGGAGTGAGAAGGGA 118

QY      2050 CCGAATTAAAGGCAA 2063
DB      119 CGGAATTAAAGGCAA 132


RESULT 5
US-10-425-114-5704
; Sequence 5704, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5704
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700470105_FLI
US-10-425-114-5704

Query Match          5.8%; Score 119; DB 13; Length 1879;
Best Local Similarity 100.0%; Pred. No. 5.5e-19; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;

1945 AAGGAGCGCGCGCCCTCTCTTCTCCACATTCTCTCGCGGGCGCTCGCTTACC 2004

```



QY 1907 ACCCGGACACCTTCCCGACACACACAGCCCAACAAAGAGGCGCGGCGCCCTCCT 1966  
Db 645 GCCCGGACACCTTCCCGACACACACAGCCCAACAAAGAGGCGCGGCGCCCTCCT 698  
QY 1967 TCCTTCTCTCCACTTCTCTCGCGGCGGCTCGCTTACCTCGCTCGCTCGCTCGCTC 2022  
Db 699 TCCTTCTCTCCACTTCTCTCGCGGCGGCTCGCTTACCTCGCTCGCTCGCTCGCTC 753

RESULT 9  
US-09-294-093B-601  
; Sequence 601, Application US/09294093B  
; Patent No. US20010051335A1  
; GENERAL INFORMATION:  
; APPLICANT: Laligudi, Raghunath, V.  
; APPLICANT: Ito, Laura, Y.  
; APPLICANT: Sherman, Bradley, K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL  
; FILE REFERENCE: PL-0009 US  
; CURRENT APPLICATION NUMBER: US/09/294,093B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 60/082,567  
; PRIOR FILING DATE: April 21, 1998  
; NUMBER OF SEQ ID NOS: 6207  
; SOFTWARE: PERL Program  
; SEQ ID NO 601  
; LENGTH: 280  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700343034H1  
; NAME/KEY: unsure  
; LOCATION: 5, 9, 13, 37, 39, 42, 46, 61, 66, 88, 196, 259, 266  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-294-093B-601

Query Match 4.0%; Score 82.6; DB 9; Length 280;  
Best Local Similarity 82.2%; Pred. No. 2.4e-10;  
Matches 88; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1948 GAGCGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2007  
Db 1 GAGCGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60

QY 2008 CTTGCGATTCGCTCGAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2054  
Db 61 NTTGCGATTCGCTCGAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 107

RESULT 10  
US-10-311-455-1354/c  
; Sequence 1354, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: PLEPNEROCK, Christian  
; APPLICANT: PLEPNEROCK, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation  
; TITLE OF INVENTION: Cytosine methylation  
; FILE REFERENCE: 5013.1014  
; CURRENT APPLICATION NUMBER: US/10/311,455  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 2424  
; SEQ ID NO 1354  
; LENGTH: 6881

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-455-1354

Query Match 3.0%; Score 62.8; DB 15; Length 6881;  
Best Local Similarity 44.2%; Pred. No. 0.0002;  
Matches 349; Conservative 0; Mismatches 437; Indels 4; Gaps 2;

QY 16 AATTCACCCCGAGTAATATCCCAATCACAATCTAAATAATGAGAGAAATATATATGCGCAT 75  
Db 6837 AATTAATCTCTTTTCTTAAATAAATAATCTTAAATAAATAAATAATTAATAATAA 6778  
QY 76 AATTATGAGCAACAAATAAATAAATGTCGCTTGAATAATGAGAGAAATATATATGCGCAT 135  
Db 6777 TTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6718  
QY 136 ACATCTCCCAAGAAATACAATCTTTTATACACAACATTAATGAGAGTCTTTTCTCTG 195  
Db 6717 ATTTTATATACAAATAATCTTTTAAATAAATAAATAAATAAATAAATAAATAA 6658  
QY 196 TAATCTCTTATTAATAAACAATTTTGGCTATTAAATAATGGCAACTAAGTTAG- -CACCA 253  
Db 6657 TAATTCAAATTTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6598  
QY 254 CTGTAATTAATTTGTCGGAACAATTTCTCTGACTAGAACCTATTGAGAGTCTCTT 313  
Db 6597 CTTTACACATTTCTTAATCTAAATTTCTATATCAAAATAAATAAATAAATAAATAA 6538  
QY 314 TTGCCBACAGTAGAATAATGGAACGCTCTTTAAATAAATAAATAAATAAATAAATAA 373  
Db 6537 ATATTAATAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6478  
QY 374 CTGTAATAAACTGAAAAATTTAGCTTTTATAGCTCTCGCTCTCTGCTAGTAGTGTAT 433  
Db 6477 CAAATATAAATAATTAACAAACAATTAATCTTCTTAAACCATCTCTATAAATAAATAA 6418  
QY 434 AAAATCAATTTTACCAATTTACCTTTTAAATAAATAAATAAATAAATAAATAAATAA 493  
Db 6417 CAAACAATTTTAAATCAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6358  
QY 494 TCAGGAGCTAAAAACAAAAAAGTTGTTCTACTGATAAAAGCAGAGATGATGACCG 553  
Db 6357 AAAACACTTTCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6298  
QY 554 TGACCGTGAGCT- -AAAGTCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 611  
Db 6297 TAAAAATTTATTTCTTATATCAATAATAAATAAATAAATAAATAAATAAATAAATAA 6238  
QY 612 TGTATTGTATGGCCTAAATACAGCACACTGACACAGTATATATTTCTCTCTCCAT 671  
Db 6237 AATAAATTTATCCAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6178  
QY 672 TATCAGGAGTAACTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 731  
Db 6177 CAAAAATTAATTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6118  
QY 732 CATTTAGCTCTACGGAATTTTATGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 791  
Db 6117 TATCTATTTCTACTATCTACTATCTACTATCTACTATCTACTATCTACTATCTACTAT 6058  
QY 792 ACTGTAAATC 801  
Db 6057 AAAATAAATC 6048

RESULT 11  
US-10-240-453-124/c  
; Sequence 124, Application US/10240453  
; Publication No. US20030148326A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA  
TITLE OF INVENTION: Transcription  
TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated  
TITLE OF INVENTION: With DNA Transcription  
FILE REFERENCE: 5013.1009  
CURRENT APPLICATION NUMBER: US/10/240,453  
CURRENT FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: PCT/EP01/03973  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 350  
SEQ ID NO 124  
LENGTH: 6881  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-240-453-124

Query Match 3.0%; Score 62.8; DB 15; Length 6881;  
Best Local Similarity 44.2%; Pred. No. 0.0002;  
Matches 349; Conservative 0; Mismatches 437; Indels 4; Gaps 2;

\* QY 16 AATTCACCCGAGTAATATCCAAATCACAATCTAAATCAGGAGAAATATATATGCCAT 75  
Db 6837 AATTATCTCTTTACCTAATAAATAATCTTAAATAAATAAATAAATAAATAAATAA 6778  
QY 76 ATTATAGAGCACTAAATAAATGCGTGTATGAAATAAATACCTATTATTAACA 135  
Db 6777 TTTAAATAAACAATATTAAATAAATAAATAAATAAATAAATAAATAAATAA 6718  
QY 136 ACATCTGCCAAGTAACAATCTTTATACACAACCTATATATGAGTCTCTTTCTCTTG 195  
Db 6717 ATTTTATATACAAATACTTTTAAATAACATAAATAATTTACCATAATTTCAATTTA 6658  
QY 196 TAACCTCTTATTAATAAACAATTTTGGCTATTAATAATGGAACCTAAGTTAG--CACCA 253  
Db 6657 TAATTTCAATTTTCAAAAAAATACTTTCCAAAAAATAAATAAATAAATAAATAA 6598  
QY 254 CTGTAAATAGATTTGTCTGCAACAATTTCTCTGACTAAGAAGCTATTTGGAGTCTCT 313  
Db 6597 CTTTACACATTTCTAATCTAATAATCTATATCAAAAAAATAAATAAATAAATAA 6538  
QY 314 TTGCCAAACAGTAGAATAATGGAACCGCTCCTTAAATAAACCATTCTCAGTCGCTGGTG 373  
Db 6537 ATATTAAATATTTTAAATAAATAATCGACTAAAAAATACTAAATAAATAAATAA 6478  
QY 374 CTGTAATAAATCTGAACATTTAGCTTTTATAGCTCTGCTCTCTGCTAGTATGCTTAT 433  
Db 6477 CAATATTAATAATTAACAACAATTAACCTATTCTTTAACCATCTTATTAATAAATA 6418  
QY 434 AAATCATTTTACCATTTACCTTTTAAATAAATGTCAGTGTAGTTTCATCAGTAGAATAC 493  
Db 6417 CAACAATTTTAACTACTATCTATCAATCAATAAATAAATAAATAAATAAATAA 6358  
QY 494 TCACGGAGCTAAACAATAAAGTTGTCTACTGATTAATAAAGCAGAGATGATGATGACCG 553  
Db 6357 AAAAAACATTTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6298  
QY 554 TGACCGTGAGCT--AAAGTCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 611  
Db 6297 TAAAAAATTTATTTCTTATATCAATAATAAATAAATAAATAAATAAATAAATAAATAA 6238  
QY 612 TGTATTGTATGGCCCTAAATTACAGCACACTGTACACACACGTATATTATTTCTCTCCAT 671

Db 6237 AATAAATTTATCCAAATAAATTTTAAATATATATCTTATAATACTAAAAATAATTCTTA 6178  
QY 672 TATCAGCAGATGTAAGTGTAAATAATTTTGTATGTTAAACATTTGTAGTAATAATTGCTAG 731  
Db 6177 CAATAATAATTTTATATAAAAAATCTTAAATTTACTCACTCGTAATAACATTAACAATA 6118  
QY 732 CATTTACGCTACGGAATTTATGAAAAAATCTAGTATTGTTTTATATAAATTTTAAATAA 791  
Db 6117 TATCTATTTCACTATATCTACATTTATAAATCTTCTTAAATTCATTTAAAAATAAATA 6058  
QY 792 ACTGTAAATC 801  
Db 6057 AAAATAAATC 6048

RESULT 12  
US-10-312-841-1/c  
Sequence 1, Application US/10312841  
Publication No. US20030186277A1  
GENERAL INFORMATION:  
APPLICANT: Epigenomics AG  
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
FILE REFERENCE: 801/1208/WO  
CURRENT APPLICATION NUMBER: US/10/312,841  
CURRENT FILING DATE: 2002-12-30  
NUMBER OF SEQ ID NOS: 2  
SEQ ID NO 1  
LENGTH: 3673778  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (3294164)  
US-10-312-841-1

Query Match 2.8%; Score 58.8; DB 15; Length 3673778;  
Best Local Similarity 44.2%; Pred. No. 0.13;  
Matches 329; Conservative 0; Mismatches 412; Indels 3; Gaps 2;

QY 49 AAAAATCAGGAGAAATATATATGCCATATTTATAGAGCAACTAAATAAATAATGCGGTGT 108  
Db 1714131 AAATATATAAATAATATATAAATAATATAAATAATATAAATAATATAAATAA 1714072  
QY 109 ATTGAAAAAACAACCTATTTATACAAACATCTGCCAAGTAACAATCTTTTATACACA 168  
Db 1714071 AATATATATAAATAATATATAAATAATATAAATAATATAAATAATATAAATAA 1714012  
QY 169 ACTTATATGTGAGTTCTTTTCTCTGTAACCTCTTATTAATAAACAATTTTGGCTATTA 228  
Db 1714011 ATATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAAATA 1713952  
QY 229 AATAATGGCAACTAAGTTAGCACCACTGTAAATAGATTTTGTCTGGCAACAATTTCTCTGA 288  
Db 1713951 AATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAAATA 1713892  
QY 289 CTAAGAAGCTATTTGGAGTCTGCTTTTGGCAACAAGTAGAAAAATGGAACCGCTCCCTAA 348  
Db 1713891 ATAT-ATAATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAA 1713833  
QY 349 AAAACCATTTCTCAATCGCTGGGTGCTGATTAATAAATGTAATAAATGTAATAAATGTA 408  
Db 1713832 AAAATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAAATA 1713773  
QY 409 CTCGCTCTCTGCTAGTGTGTATAAATAATCATTTTACCAATTTACCTTTTAAATAAAT 468  
Db 1713772 AAAATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAAATA 1713713  
QY 469 TACGTAGTTTTCATCAGTAGAATCTACTCAGGAGCTAAACCAAAAAAGTTGTTCTACTGA 528  
Db 1713712 ATATATAATAAATAATATAAATAATATAAATAATATAAATAATATAAATAAATA 1713653

QY 529 TAAAGCAGAGATGATGATGACCGGTGAGCTAAAGTCCAAAAAATAAACTGCT 588  
Db 1713652 ATATATAAATATATATAAATAATATAAATAATATAAATAATATAAATAA 1713593  
QY 589 CCACAATACGACAAAACAAAGTTGATGATGATGATGATGATGATGATGATG 648  
Db 1713592 ATATATAAATATATATAAATAATATAAATAATATAAATAATATAAATA 1713533  
QY 649 CACGATATATATCTCTCTCCATATACAGGATGATGATGATGATGATGATG 708  
Db 1713532 TATATAAATATATATAAATAATATAAATAATATAAATAATATAAATA 1713475  
QY 709 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 768  
Db 1713474 ATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1713415  
QY 769 TTGTTTAT 792  
Db 1713414 ATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1713391

RESULT 13  
US-10-240-453-287/c  
; Sequence 287, Application US/10240453  
; Publication No. US20030148326A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA  
; TITLE OF INVENTION: Transcription  
; TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated  
; TITLE OF INVENTION: With DNA Transcription  
; FILE REFERENCE: 5013.1009  
; CURRENT APPLICATION NUMBER: US/10/240,453  
; CURRENT FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: PCT/EP01/03973  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 350  
; SEQ ID NO 287  
; LENGTH: 5362  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-240-453-287

Query Match 2.8%; Score 53; DB 15; Length 5362;  
Best Local Similarity 42.8%; Pred. No. 0.05;  
Matches 326; Conservative 0; Mismatches 430; Indels 5; Gaps 1;  
QY 49 AAAAAATCAGGAGAAATATATATGATGATGATGATGATGATGATGATGATG 108  
Db 4846 AATATCCGAAATATTTCTATATACCATCTTAACAAATCGCAAACTTAATCATCATCT 4787  
QY 109 ATTGAAAAAACCCTATTTATTAACAAACATCTGCCAGAAATACAAATCTTTTATAC 168  
Db 4786 AAAAAATACAACTACAAAAAACCCTTCTTCTTAAACCGGCAAACTACTATAAAT 4727  
QY 169 ACTTATATGAGTCTCTTTCTCTGTAACCTCTTATTAATAAACAATTTTGGCTATTA 228  
Db 4726 ACTATACTATTAACAATAAACCAGGTAATTTCTTATTAATAAACAATCTTTAGCTCT 4667  
QY 229 AATAATGCAACTAAGTTAGCAACCACTGTAATTTGTTCTGGAACAATTTCTCTGA 288

Db 4666 CTTATCCCAAACTAAAAATATATATATATATATATATATATATATATATAT 4607  
QY 289 CTAAAGAGCTATTTGACGTCTCTTTTGGCAACAAGTAGAATAAGCAACCGCTCTTAA 348  
Db 4606 CTATACCTTATCTTTAAACAAACGTAATATATATATATATATATATATATATAT 4547  
QY 349 AAAACCAATCTCATCGCTGGGTGCTGATATAAACTGAA-----AACATTAGCTTTT 403  
Db 4546 TCACCAATAAAAAACATAAAAAACTTCTTAAACCTTACACCAAAATTTCTTTCAA 4487  
QY 404 TAGCTCTCGCTCTCTCTGCTAGTATGTTTATAAAATCATTTTACCATAATACCTTTTAA 463  
Db 4486 AAACCAACAACTTAAATTAACATACGATTAATAAACAATAATCAATTTTAAAAAT 4427  
QY 464 AACTGTACGTAGTTTCTATCAGTAGAAGTCTACGAGGCTTAAACAAAAAGTTTGTCT 523  
Db 4426 ATAAACTCCCTACCTATATATCCAACTACTAAAAAACTTAAACAAAAATTCGGCTTA 4367  
QY 524 ACTGATAAAAGCAGAGATGATGATGACCGGTGAGCTAAAGTCCAAAAAATAAAAA 583  
Db 4366 ACCGAAAAACGAAACTTAATTAACGTAATAAATAACACTATATATCCCACTAC 4307  
QY 584 CTGCTCCACAATAACGACAAACAAAGTTGTTATGATGCGCTTAAATACAGCACACTGA 643  
Db 4306 CTAATAAACTAAACAAACAAATTAACCCGAAAAACGAAAAATACACGAAACCGA 4247  
QY 644 CACCACACGTATATTCTCTCTCCATATATCAGGATGATGATGATGATGATGATG 703  
Db 4246 AATCTTACCTACACTCTCCATCTAAATAAACAACAAACGAACTCTATCTCAAAAA 4187  
QY 704 GTTAAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 763  
Db 4186 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 4127  
QY 764 TAGTATTTTAT 804  
Db 4126 ATTCTTCTCCCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 4086

RESULT 14  
US-10-221-613-390/c  
; Sequence 390, Application US/10221613  
; Publication No. US20040029123A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle  
; FILE REFERENCE: 5013.1004  
; CURRENT APPLICATION NUMBER: US/10/221,613  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: PCT/EP01/02945  
; DE 10013847.00  
; DE 10019058.8  
; DE 10019173.8  
; DE 10032529.7  
; DE 10043826.1  
; PRIOR FILING DATE: 2001-03-15  
; 2000-03-15  
; 2000-04-06  
; 2000-04-07  
; 2000-06-30  
; 2000-09-01  
; NUMBER OF SEQ ID NOS: 428  
; SEQ ID NO 390  
; LENGTH: 19380  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-221-613-390







```

RESULT 3
US-09-313-294A-4684
; Sequence 4684, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4684
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 70034858H1
; NAME/KEY: unsure

```

	Query Match	3.0%;	Score 62.4;	DB 1;	Length 7218;
	Best Local Similarity	0.8%;	Pred.No. 9.2e-08		
	Matches	3;	Conservative 234;	Mismatches 135;	Indels 0; Gaps 0
QY	1652	GGTATCCTATCCATGTGTCACAGTCCACAGAGTACGCTACTGCCGAGGCCGACG	1711		
DB	1064	GATTT	112		

US-09-596-196-2/c  
; Sequence 2, Application US/09596196  
; Patent No. 6586390  
; GENERAL INFORMATION:  
; APPLICANT: Haley, Dana A  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ho, Alice S  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Tillinghast, John S  
; APPLICANT: Sinku, Ankura  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Dmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL  
; TITLE OF INVENTION: PROTHROMBINASE-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: HYS-14  
; CURRENT APPLICATION NUMBER: US/09/596,196  
; CURRENT FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-596-196-2

Query Match 2.3%; Score 47.4; DB 4; Length 1069;  
Best Local Similarity 46.6%; Pred. No. 0.00078;  
Matches 186; Conservative 0; Mismatches 211; Indels 2; Gaps 1;

QY 48 TAAAAATCAGGAGAAATATATGCCCATTATATGCCCATTATATGAGCAAGCACTAAATATAAATGTGGTTG 107  
Db 996 TTAATATCATTAATATTTAGGAAGCAAGTGTAGTTCCTTGAACCAATTTTCATTG 937  
QY 108 TATTGAAAAAACCCTATTATTAACAACAATCTGCCAAGATACATTTCTTTATACAC 167  
Db 936 TATATTGTTAATATAGTCAGAAGTAAACACATACATAAGCCATGTTTCTTTTATAGAA 877  
QY 168 AACTTATATGTGAGTCTCTTTCTTGTAACTCTTATTAATAAACAATTTTGGCTATT 227  
Db 876 TACTACAAAT--TGAAGTCTTCTAATAAATCAATCAATCAATCAATCAATCAATCAAT 819  
QY 228 AAATAATGGCAACTAAGTACCACTGTAAATAGATTTTGTCTGGAACAATTTCTCTG 287  
Db 818 AAATTTGGCTTAATATGTTGAAACACTAAGTGAAGAAAGATAAACTTTTAAATACTTTAA 759  
QY 288 ACTAAGAAGCTATTGGAGTCTCTTTTGGCAACAAGTAGAAAATGGAACCGCTCCTTA 347  
Db 758 TATATTATCATTTGAGAACTTGCATTACAATGTTAAATGAGATTATTTAAATATGGAAT 699  
QY 348 AAAAACCATTTCTCATCGCTGGTGGTGAATAAATACTGAAACATTTAGCTTTTATAGC 407  
Db 698 GTACATCTTCTAATTTTCATTGAAACAGATTAACTCTGCAGGTCAGTTGTTTGGT 639  
QY 408 TCTGCTCTGCTGATGATGTTTATATAATCAATTTTAC 446  
Db 638 CCAGTGGCCCAATTTCAATTCAGTTGCAAGCAATTTTCC 600

RESULT 7  
US-09-596-196-3/c  
; Sequence 3, Application US/09596196  
; Patent No. 6586390  
; GENERAL INFORMATION:  
; APPLICANT: Haley, Dana A  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ho, Alice S  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y. Tom

US-09-593-995-10/c  
; Sequence 10, Application US/09593995  
; Patent No. 6406888  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: HELICAL CYTOKINE ZALPHA33  
; FILE REFERENCE: 99-38  
; CURRENT APPLICATION NUMBER: US/09/593,995  
; CURRENT FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: 60/139,121  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 20598  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-593-995-10

Query Match 2.3%; Score 47.8; DB 4; Length 20598;  
Best Local Similarity 49.4%; Pred. No. 0.0053; Indels 0; Gaps 0;  
Matches 124; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 27 AGTAAATATCCAAATCAATCTAAATCAGGAGAAATATATGCGCATATTTATAGAAGC 86  
Db 8561 AGTTAAAAACAAGTACAGTTTAAAAAAGTGAATCTGATGATTTTATGTTGAAGA 8502  
QY 87 AACTAAATAAATGCGTGTGTTGAAAAAACCCTATTATACAACAATCTGCCAA 146  
Db 8501 AAATGAAGATATATGCGTGTGTTGAAAAAATTTCTCAAAATGCTTAACTCTGATAA 8442  
QY 147 GAATACAATTTCTTTATACACAATTTATGTCAGTTCTTTTCTCTCTGTAAGTCTTATT 206  
Db 8441 GATAATTAAGATGCTTAAAGCATACATTAAATATAAAGTCTGATTTAAAGTTTACTT 8382  
QY 207 AATAAACAATTTTGGCTATTAATAATGCAACTAAGTTAGCACCATCTGTAATAGATT 266  
Db 8381 AAAAAATCAATAGCAGGAGATATGGTGCATCTATCTATGTAACACCATTAATAAATTA 8322  
QY 267 TTGTCGTGAAC 277  
Db 8321 TTACAGTAAC 8311

RESULT 6

```

; APPLICANT: Tillinghaast, John S
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenchua
; APPLICANT: Dmanac, Radole T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL
; TITLE OF INVENTION: PROTHROMBINASE-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-14
; CURRENT APPLICATION NUMBER: US/09/596,196
; CURRENT FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1167)
; US-09-596-196-3

Query Match      2.3%; Score 47.4; DB 4; Length 2013;
Best Local Similarity 46.6%; Pred. No. 0.0013;
Matches 186; Conservative 0; Mismatches 211; Indels 2; Gaps 1;

QY 48 TAAAAATCGGAGAAATATATATGCGCATATATAGAACCACTAAATAAATGTCGGTTG 107
DB 1447 TTAATAATCACTAATAATTTTAGGACACAGTTGATGTTCACTTGAACAAATTTTCATTG 1388
QY 108 TATTGAAAAAAACCTATTATTAACAACATCTGCCAGATACATAATCTTTTATACAC 167
DB 1387 TATATGTTAATATAGTCAGAGTAATAACATACATAAGCCATGTTTCTTTTATAGAA 1323
QY 169 AACTATATGTCAGTTCTTTTCTCTGTTGTAACCTTATTAATAAACAATTTTGGCTATT 227
DB 1327 TACTACAAAT--TGAAGTTTCTAATTAACCTCAATCAATCAATGCAATGCAATGTT 1270
QY 228 AATAATGCGCACTAGTTAGCACCCTCTAATATAGATTTCTCTGGAACAATTTCTCTG 287
DB 1269 AATTTTGGCTATATGTTTGAACACTAAGTGAAGAAAGATAAATTTTAAATCTTTAA 1210
QY 288 ACTAAGAAGCTATTGTCATGTCCTTTTCCCAACCAAGTAGAAATGGAACCGCTCCTTA 347
DB 1209 TATATATCATTTGTAGAACTTGCATTACAAATGTGTTAAATGAGATTATTTAAATATG 1150
QY 348 AAAAACCATTCTCACATCGCTGGTCTGTAATAAACTGAAACATTAAGCTTTTATAGC 407
DB 1149 GTACATCTTCTAATTTTCAATGAAACAGATTATCTTTGACAGGTGAGTTGTTTGGT 1090
QY 408 TCTGCTCTCTGCTAGTATGTGTTATAAAATCATTTTAC 446
DB 1089 CCAGTGGCCCACTGAATTCAGTTCCAGTTGCAAGCAATTTTCC 1051

RESULT 8
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HAYTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7

```

```

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640661
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

Query Match      2.2%; Score 44.8; DB 4; Length 640661;
Best Local Similarity 48.8%; Pred. No. 0.55;
Matches 121; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 76 ATTATAGAACCACTAAATAAATGTCGGTGTATTGAAAAAACAACCTATTATACAA 135
DB 294683 AATTTAACACCACTTTAACTACATTCATCTCTGCGGAGATAAAATATGAAGATGACCAA 294742
QY 136 ACATCTGCCAAGATACAAATCTTTTATACACAACTTATATGTCAGTTCTTTTCTCTTG 195
DB 294743 ATAAAGATTTTAATCAAAATGTTAAATTAAGAAGATGAAGTTTATTTTAATAAGAG 294802
QY 196 TAACTCTTATTAATAAAACATTTTGGCTATTTAATAATGCGCAACTAAGTTAGCACT 255
DB 294803 TTAATCTAAATTTTGAAGAAATTTTATATCAACAGTAATTAATAAATAATTCATAA 294862
QY 256 GTAAATTAGATTTGTCGGAACAATTTCTCTCACTAAGAAGCTATTGGAAGTGTCTTTT 315
DB 294863 TAAATTTGTTTTTTTATCTTAATTTTCTCCGTATAAGAAATTTTAAAGTTAATTTT 294922
QY 316 GCCAAACA 323
DB 294923 AACATATA 294930

RESULT 9
US-10-204-708-51/c
; Sequence 51, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 51
; LENGTH: 5219
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-204-708-51

Query Match      2.1%; Score 43.6; DB 4; Length 5219;
Best Local Similarity 46.0%; Pred. No. 0.036;
Matches 148; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 374 CTGAATAAACTGAAACCAATAGCTTTTATAGCTCTCGCTCTGCTAGTATGTGTAT 433
DB 4298 CTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4299
QY 434 AAATCATTTTACCAATTAACCTTTTAAATAAATGTCAGTATGTTTATCATGAGAACTAC 493

```



Db 23 WGMVTRGSKSWRAKWSMMKRRRRRAWWKSMCMKSKGKSWRSGMWTKRMKGRGA 82  
QY 1529 COTGATAGCAITTTGATTCGTTCAATTTGAACCTGTTTAACTTATATATAGTAGAA 1588  
Db 83 ASWAGTSMWMTYTRRYYRKAACCTKRAAGWAGWAGWAGWAGWAGWAGWAGWAGWAG 142  
QY 1589 ATTAGTCCAACTCATCTCTTAATAAAGATATAAACCACATCGAATTTAAGAAATTATGATA 1648  
Db 143 YWAMKSKESMRRRRRAWWYMMARRTMMGRASCYRGAYMASAGMYMMYMMYMERK 202  
QY 1649 GCAGGTATCTATCATCTGTCATCGCTCACAGTCACAGAGGTAGCACTGCGGCGCG 1708  
Db 203 WMSYAGSWMRKWTTRRCASYSWSSYCMGAKOMWTKISRSWYSYRCKYRSRCC 262  
QY 1709 AGCGCTCCCATTTGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1768  
Db 263 WMSYCWYKTYRSWYSCYKTKRASCCMMCMKWKWKWMMYMMYMMYCKTKTSAM 322  
QY 1769 TTCGGCAAT 1778  
Db 323 RYRSCYSAK 332

RESULT 13  
US-09-621-976-2813/C  
; Sequence 2813, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET 054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 2813  
; LENGTH: 832  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 235..399  
US-09-621-976-2813

Query Match 2.0%; Score 41.2; DB 4; Length 832;  
Best Local Similarity 13.4%; Pred. No. 0.049;  
Matches 54; Conservative 173; Mismatches 176; Indels 1; Gaps 1;  
QY 110 TTGAAAAAAGCACTATTATACAAACATCTCCCAAGATACAAATCTTTTATACACAA 169  
Db 405 TTGCTAAAGTACAAAGATCTACCAATAATAATTATTTTGTYYTMMKTKWYMTYTM 346  
QY 170 CTTATATGTGATCTTTTCTCTGTAAGTCTTATTAATAACATTTTGGCTATTAA 229  
Db 345 TRMMWKKKARWYWKSYACASRYKTYGWWMMKRRMSTRYCMCKWCKNYK 286  
QY 230 ATAATGCAACTAAGTTAGCACCCTGTATTAATTAGATTTTCTGGAACAATTTCTGTAC 289  
Db 285 RRCAYTMMGRMWSYAWGKWSMRSMSCTRMYYKKGSTYMTKCTCATWYWKY 226  
QY 290 TAAGAACCTATTGGATCTCTTTTCCCAACAAAGTAGAAATGGACCGCTCTTAA 349  
Db 225 KRMWSKTCWSGSGGYTSTYSTRYSMY-WASMMYTCMWWGRWSTYMMYMWANGKKWR 167  
QY 350 AAACCATCTCACATCGCTGGTCTGAATAAATAAAGCAATTAAGCTTTTATAGCTC 409  
Db 166 YATTTWRAMWMAWMTMMYMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 107  
QY 410 TCGCTCTCTGATGTTGTTTATAAATCATTTTACCATTACCTTTTAAATACTGT 469  
Db 106 WAYAWKTRSYWCWRWKRKRCMMWMMWMAWYKTMWMMWMMWMMWMMWMMWMMWMMWMM 47

QY 470 ACCTAGTTTCATCAGTAGAAGTACTACGAGCTAAACAAAA 513  
Db 46 MMMYYWYWRAMKRRMMWKRWSWSMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMW 3  
RESULT 14  
US-08-439-814-3  
; Sequence 3, Application US/08439814  
; Patent No. 5968735  
; GENERAL INFORMATION:  
; APPLICANT: STEIN, Ulrike  
; APPLICANT: WALTHER, Wolfgang  
; TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF  
; TITLE OF INVENTION: THERAPY-RELEVANT GENES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIKAI, DO, MARCELSTEIN, MURRAY & ORAM LLP  
; STREET: 655 Fifteenth Street, N. W., Suite 330 G  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,814  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 4238778.7  
; FILING DATE: 12-NOV-1992  
; PRIOR APPLICATION DATA: DE PCT/DE93/01086  
; FILING DATE: 10-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KLESNER, Sharon N.  
; REGISTRATION NUMBER: 36,335  
; REFERENCE/DOCKET NUMBER: P1614-5015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/638-5000  
; TELEFAX: 202/638-4810  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30B (EPO)  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4238778.7  
; FILING DATE: 12-NOV-1992  
; PRIOR APPLICATION DATA:  
; FILING DATE: 10-NOV-1993  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1318 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-439-814-3  
Query Match 2.0%; Score 41; DB 2; Length 1318;  
Best Local Similarity 63.9%; Pred. No. 0.08;  
Matches 62; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 702 ATGTTAAACATTTGTAGTAAATATTGCTAGCATTTAGCTTACGAAATTTTATGAAAAA 761  
Db 462 ATATTAAATGTTGGCAGTATATATGGAAGAAATACAACTAATGTAATATGCTAAAAACA 521

**Qy**           762 TGTAGTATTGTTTTATATAAATTTTAATAAACTGTAA 798  
             ||| ||| ||| ||| ||| ||| ||| |||  
**Dδ**           522 TGCTATGTTTATTTTACTAATTTGAATTAATAATGTAA 558

RESULT 15  
US-08-439-814-2

```

RESULT 15
US-08-439-814-2
; Sequence 2, Application US/08439814
; Patent No. 5968735
; GENERAL INFORMATION:
; APPLICANT: STEIN, Ulrike
; APPLICANT: WALTHER, Wolfgang
; TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
; TITLE OF INVENTION: THERAPY-RELEVANT GENES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 G
; STREET: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/439,814
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 4238778.7
; FILING DATE: 12-NOV-1992
; APPLICATION NUMBER: DE PCT/DE93/01086
; FILING DATE: 10-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KLESNER, Sharon N.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: P1614-5015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B (BPO)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4238778.7
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE93/01086
; FILING DATE: 10-NOV-1993
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1688 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-439-814-2

Query Match 2.0%; Score 41; DB 2; Length 1688;
Best Local Similarity 63.9%; Pred. No. 0.096;
Matches 62; Conservative 0; Mismatches 35; Indels 0; Gaps 0

Qy 702 ATGTTAAACATTGTAGTAATATTTGGCTAGCAATTCCTACGGAAATTTATGAAAAA 761
Db 832 ATATTAAATGTTGGCAGTAAATATGGAAGGAATTTACAACTAATGTAATATGCTAAAA 891

```